

Search Nts for 10/603108

<!--StartFragment-->GenCore version 5.1.9

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 26, 2006, 16:55:33 ; Search time 751 Seconds
(without alignments)
9218.965 Million cell updates/sec

Title: US-10-603-108-1298
Perfect score: 993
Sequence: 1 atgctaactttaacagttga.....ccaaaaaaaaatcaagtttag 993

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 8

Total number of hits satisfying chosen parameters: 5740404

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	993	100.0	993	12 ADL03612	Adl03612 DNA encod
2	793	79.9	269223	4 AAF28554	Aaf28554 Genomic f
3	790	79.6	1359	8 ACA38948	Aca38948 Prokaryot
4	648	65.3	1119	12 ADL03329	Adl03329 DNA encod
5	21	2.1	474	10 ACC61620	Acc61620 Gene sequ

	6	21	2.1	474	10	ADK64341	Adk64341 Disease t
	7	20	2.0	60	6	ABN34683	Abn34683 Human spl
	8	20	2.0	425	9	ACH13849	Ach13849 Human adu
	9	20	2.0	496	9	ACH44169	Ach44169 Human foe
	10	20	2.0	557	6	ABQ36870	Abq36870 Oligonucl
c	11	20	2.0	557	6	ABQ36871	Abq36871 Oligonucl
	12	20	2.0	1024	6	ABQ54770	Abq54770 Human ova
	13	20	2.0	1371	4	AAS53339	Aas53339 Haemophil
	14	20	2.0	1371	8	ACA34196	Aca34196 Prokaryot
	15	20	2.0	1371	11	ADL46421	Adl46421 UDP-N-ace
	16	20	2.0	1371	14	AEC10850	Aec10850 Haemophil
	17	20	2.0	1455	3	AAC98882	Aac98882 Human pan
	18	20	2.0	1708	4	AAI60145	Aai60145 Human pol
	19	20	2.0	2007	4	AAI58359	Aai58359 Human pol
	20	20	2.0	2007	5	ADQ98568	Adq98568 DNA encod
	21	20	2.0	2007	9	ADB48328	Adb48328 Novel hum
	22	20	2.0	2850	15	AEE31211	Aee31211 Haemophil
	23	20	2.0	2880	15	AEE31400	Aee31400 Haemophil
	24	20	2.0	25523	13	ADT05538	Adt05538 Haemophil
c	25	20	2.0	106645	13	ADT05645	Adt05645 Haemophil
	26	20	2.0	110000	2	AAT42063_06	Continuation (7 of
c	27	19	1.9	688	4	ABL22443	Abl22443 Drosophil
	28	19	1.9	1434	8	ACA34455	Aca34455 Prokaryot
	29	19	1.9	2379	6	ABS67350	Abs67350 Chlamydia
	30	19	1.9	2379	10	ADD43761	Add43761 Chlamydia
	31	19	1.9	2379	14	AEA19053	Aea19053 Chlamydia
	32	19	1.9	3485	4	ABL22442	Abl22442 Drosophil
c	33	19	1.9	3780	13	ADS89656	Ads89656 Oligonucl
	34	19	1.9	4333	4	ABL07040	Abl07040 Drosophil
	35	19	1.9	8200	4	ABL07024	Abl07024 Drosophil
	36	19	1.9	9302	13	ADT05516	Adt05516 Haemophil
c	37	19	1.9	9524	6	ABK39993	Abk39993 Human che
c	38	19	1.9	9524	6	ABL32838	Abl32838 Human imm
	39	19	1.9	15147	13	ADT05641	Adt05641 Haemophil
c	40	19	1.9	15853	6	ABL70466	Abl70466 Chemicall
c	41	19	1.9	15853	6	AAS61457	Aas61457 Human gen
c	42	19	1.9	80321	11	ACN45012	Acn45012 Mouse gen
c	43	19	1.9	110000	2	AAT42063_08	Continuation (9 of
	44	19	1.9	110000	2	AAT42063_14	Continuation (15 o
c	45	19	1.9	110000	5	AAI61373_3	Continuation (4 of

<!--EndFragment-->

<!--StartFragment-->GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 26, 2006, 17:09:12 ; Search time 5793 Seconds
 (without alignments)
 10961.469 Million cell updates/sec

Title: US-10-603-108-1298
 Perfect score: 993
 Sequence: 1 atgctaactttaacagttga.....ccaaaaaaatcaagtttag 993

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 8

Total number of hits satisfying chosen parameters: 10367082

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : GenEmbl:*
 1: gb_env:*
 2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	993	100.0	993	2	AR450634	AR450634 Sequence
2	793	79.9	269223	2	AR408762	AR408762 Sequence
3	793	79.9	269223	2	AX067466	AX067466 Sequence
4	648	65.3	1119	2	AR450351	AR450351 Sequence
5	23	2.3	165217	12	CT027727	CT027727 Danio rer

	6	23	2.3	214513	11	BX950853	BX950853 Zebrafish
c	7	22	2.2	164550	5	CNS01RHY	AL162633 Human chr
	8	22	2.2	175988	5	CNS05TC7	AL355073 Human chr
c	9	22	2.2	198278	12	AC010097	AC010097 Homo sapi
	10	22	2.2	213316	12	AC160948	AC160948 Bos tauru
c	11	22	2.2	233753	12	AC137805	AC137805 Homo sapi
	12	21	2.1	474	2	AX596368	AX596368 Sequence
	13	21	2.1	474	2	AX820660	AX820660 Sequence
	14	21	2.1	474	2	AX831690	AX831690 Sequence
c	15	21	2.1	868	4	SCYGR076C	Z72861 S.cerevisia
	16	21	2.1	1449	4	SCYMR26	X56106 S.cerevisia
c	17	21	2.1	110000	4	AP008216_190	Continuation (191
c	18	21	2.1	110000	4	AE016959_190	Continuation (191
	19	21	2.1	110000	4	AP007159_09	Continuation (10 o
	20	21	2.1	115023	4	AC138527	AC138527 Medicago
	21	21	2.1	119370	12	AC105930	AC105930 Magnaport
	22	21	2.1	151991	4	AC091122	AC091122 Oryza sat
	23	21	2.1	167152	6	AC163393	AC163393 Mus muscu
c	24	21	2.1	168536	12	AC162268	AC162268 Bos tauru
c	25	21	2.1	173239	5	AC016399	AC016399 Homo sapi
	26	21	2.1	176188	5	AC068898	AC068898 Homo sapi
c	27	21	2.1	186014	11	BX908749	BX908749 Zebrafish
	28	21	2.1	192706	12	AC173393	AC173393 Bos tauru
c	29	21	2.1	208154	11	CR788244	CR788244 Zebrafish
	30	21	2.1	215498	11	BX547927	BX547927 Zebrafish
	31	21	2.1	223952	6	AC107742	AC107742 Mus muscu
c	32	21	2.1	254436	13	AE014827	AE014827 Plasmodiu
	33	20	2.0	60	2	CQ537796	CQ537796 Sequence
	34	20	2.0	687	13	CT033675	CT033675 Platynere
c	35	20	2.0	687	13	CT033676	CT033676 Platynere
	36	20	2.0	699	13	CT032677	CT032677 Platynere
	37	20	2.0	704	13	CT032567	CT032567 Platynere
c	38	20	2.0	704	13	CT032568	CT032568 Platynere
c	39	20	2.0	720	13	CT032678	CT032678 Platynere
c	40	20	2.0	1221	13	AY039360	AY039360 Onthophag
	41	20	2.0	1368	2	CS222758	CS222758 Sequence
	42	20	2.0	1371	2	AX932186	AX932186 Sequence
	43	20	2.0	2007	2	AR338747	AR338747 Sequence
	44	20	2.0	2109	5	AK026760	AK026760 Homo sapi
	45	20	2.0	2222	5	AK124047	AK124047 Homo sapi

<!--EndFragment-->

<!--StartFragment-->GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 26, 2006, 17:44:59 ; Search time 5675 Seconds
(without alignments)
9784.651 Million cell updates/sec

Title: US-10-603-108-1298
Perfect score: 993
Sequence: 1 atgctaactttaacagttga.....ccaaaaaaatcaagtttag 993

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 8

Total number of hits satisfying chosen parameters: 94430840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
c	1	23	2.3	289	14	CT011940	CT011940 KBrH119N1
c	2	23	2.3	367	14	CT012055	CT012055 KBrH119N1
c	3	23	2.3	907	13	DU114572	DU114572 KBrH096K1
c	4	22	2.2	671	9	DN537400	DN537400 1373575 M
	5	22	2.2	717	9	DN535975	DN535975 1372039 M
	6	22	2.2	721	10	DT891184	DT891184 1472302 M

c	7	22	2.2	729	10	DT889825	DT889825 1470766 M
	8	22	2.2	797	10	DV183743	DV183743 CT026_F03
c	9	21	2.1	379	14	T09797	T09797 0378m7 gmbP
c	10	21	2.1	426	13	CW448297	CW448297 fsbb001f1
c	11	21	2.1	669	13	CW059644	CW059644 104_302_1
c	12	21	2.1	686	8	CV718881	CV718881 UCRCS08_0
	13	21	2.1	690	8	CV718880	CV718880 UCRCS08_0
c	14	21	2.1	694	13	CW435175	CW435175 fsbb001f1
c	15	21	2.1	744	10	DW581574	DW581574 EST_ssal_
c	16	21	2.1	757	13	DU127507	DU127507 KBrH108M2
	17	21	2.1	761	8	CX075188	CX075188 UCRCS08_4
	18	21	2.1	770	11	AZ210845	AZ210845 SP_0153_B
c	19	21	2.1	775	8	CX047009	CX047009 UCRCS09_1
	20	21	2.1	806	8	CX047008	CX047008 UCRCS09_1
c	21	21	2.1	812	8	CX053775	CX053775 UCRCS09_8
	22	21	2.1	816	8	CX053774	CX053774 UCRCS09_8
c	23	21	2.1	877	12	CG956559	CG956559 MBEKJ23TR
	24	21	2.1	1210	14	AG323994	AG323994 Mus muscu
	25	20	2.0	277	8	CN824930	CN824930 96 Nicoti
	26	20	2.0	350	7	BE170924	BE170924 QV3-HT054
c	27	20	2.0	360	1	AM142296	AM142296 AM142296
	28	20	2.0	362	1	AV659387	AV659387 AV659387
c	29	20	2.0	369	2	BF756568	BF756568 QV3-CT055
	30	20	2.0	376	10	DR900809	DR900809 JGI_XZT54
c	31	20	2.0	377	8	CO987375	CO987375 UMC-pd10e
	32	20	2.0	399	4	BY396352	BY396352 BY396352
c	33	20	2.0	418	1	AV670216	AV670216 AV670216
	34	20	2.0	424	7	AW802965	AW802965 IL2-UM007
c	35	20	2.0	427	1	AM155260	AM155260 AM155260
c	36	20	2.0	433	1	AU179366	AU179366 AU179366
	37	20	2.0	444	1	AI393324	AI393324 tg44a08.x
c	38	20	2.0	449	14	AL754153	AL754153 Arabidops
	39	20	2.0	462	4	BW571097	BW571097 BW571097
c	40	20	2.0	487	4	BX112993	BX112993 BX112993
c	41	20	2.0	489	8	CX103703	CX103703 BI027C21
	42	20	2.0	490	12	CG065161	CG065161 PUIBY17TB
	43	20	2.0	537	9	DA841670	DA841670 DA841670
	44	20	2.0	540	13	CW105344	CW105344 104_474_1
c	45	20	2.0	550	1	AV669211	AV669211 AV669211

<!--EndFragment-->

<!--StartFragment-->GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: December 26, 2006, 15:16:56 ; Search time 203 Seconds
 (without alignments)
 743.258 Million cell updates/sec

Title: US-10-603-108-3218
 Perfect score: 1692
 Sequence: 1 MLTLTVDKPFGLGRIVRNQG.....LARAKQATIIGWSRPKKNQV 330

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1692	100.0	330	8	ADL05532	Adl05532 M. catarr
2	1669	98.6	453	6	ABU35078	Abu35078 Protein e
3	1242	73.4	372	8	ADL05249	Adl05249 M. catarr
4	965	57.0	454	6	ABU16817	Abu16817 Protein e
5	965	57.0	461	6	ADA33820	Ada33820 Acinetoba
6	891	52.7	458	6	ABU39487	Abu39487 Protein e
7	877	51.8	456	4	AAU35480	Aau35480 Haemophil
8	877	51.8	456	6	ABU30326	Abu30326 Protein e
9	877	51.8	456	7	ADL46422	Adl46422 UDP-N-ace
10	877	51.8	456	9	AEC10851	Aec10851 Haemophil

11	877	51.8	456	10	AEE31345	Aee31345 Haemophil
12	875	51.7	453	6	ABU49642	Abu49642 Protein e
13	873	51.6	456	7	ADL46424	Adl46424 UDP-N-ace
14	873	51.6	456	9	AEC10853	Aec10853 Haemophil
15	862	50.9	456	6	ABU50612	Abu50612 Protein e
16	855.5	50.6	457	6	ABU41088	Abu41088 Protein e
17	855.5	50.6	493	7	ADF07235	Adf07235 Bacterial
18	854	50.5	380	8	ADI38913	Adi38913 N-termina
19	854	50.5	456	4	AAU34807	Aau34807 E. coli c
20	854	50.5	456	6	ABU28830	Abu28830 Protein e
21	854	50.5	456	8	ADI38911	Adi38911 glmU, SEQ
22	839	49.6	458	6	ABM70564	Abm70564 Photorhab
23	837	49.5	456	6	ABU28357	Abu28357 Protein e
24	832	49.2	456	6	ABU48227	Abu48227 Protein e
25	827	48.9	456	4	AAU38471	Aau38471 Salmonell
26	827	48.9	458	4	AAU36166	Aau36166 Klebsiell
27	827	48.9	458	6	ABU31195	Abu31195 Protein e
28	827	48.9	474	7	ABO64180	Abo64180 Klebsiell
29	815.5	48.2	461	9	AEB42140	Aeb42140 L. pneumo
30	812.5	48.0	425	6	ABU33617	Abu33617 Protein e
31	809.5	47.8	456	8	ADP08171	Adp08171 Neisseria
32	802.5	47.4	471	6	ABU37628	Abu37628 Protein e
33	797.5	47.1	456	6	ABU37751	Abu37751 Protein e
34	791.5	46.8	471	6	ABP77136	Abp77136 N. gonorr
35	791.5	46.8	471	6	ABU37558	Abu37558 Protein e
36	779.5	46.1	453	6	ABU19390	Abu19390 Protein e
37	778.5	46.0	406	6	ABU40340	Abu40340 Protein e
38	769.5	45.5	455	6	ABU41713	Abu41713 Protein e
39	766.5	45.3	566	6	ABU22204	Abu22204 Protein e
40	762.5	45.1	457	6	ABU23281	Abu23281 Protein e
41	759.5	44.9	453	6	ABU21474	Abu21474 Protein e
42	752.5	44.5	454	4	AAU36519	Aau36519 Pseudomon
43	752.5	44.5	454	6	ABU38925	Abu38925 Protein e
44	752.5	44.5	462	7	ABO70256	Abo70256 Pseudomon
45	697	41.2	409	6	ABU31446	Abu31446 Protein e

<!--EndFragment-->

<!--StartFragment-->GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: December 26, 2006, 15:17:35 ; Search time 303 Seconds
 (without alignments)
 1007.443 Million cell updates/sec

Title: US-10-603-108-3218
 Perfect score: 1692
 Sequence: 1 MLTLTVDKPFGLGRIVRNQG.....LARAKQATIIGWSRPKKNQV 330

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1069.5	63.2	458	2	Q4FPY8_PSYAR	Q4fpy8 psychrobact
2	1054.5	62.3	458	2	Q3GS42_9GAMM	Q3gs42 psychrobact
3	939	55.5	454	2	Q6F6U9_ACIAD	Q6f6u9 acinetobact
4	927.5	54.8	452	2	Q2S6P3_9GAMM	Q2s6p3 hahella che
5	909.5	53.8	454	2	Q36LW9_MARHY	Q36lw9 marinobacte
6	893	52.8	462	2	Q2YCA1_NITMU	Q2ycal nitrosospir
7	891	52.7	458	2	Q9CK29_PASMU	Q9ck29 pasteurella
8	889	52.5	454	2	Q2X1G8_9GAMM	Q2x1g8 shewanella
9	889	52.5	454	2	Q2ZQL4_SHEPU	Q2zql4 shewanella
10	887	52.4	457	2	Q65R54_MANSM	Q65r54 mannheimia
11	886	52.4	452	2	Q3IK30_PSEHT	Q3ik30 pseudoalter
12	885	52.3	454	2	Q8E8C2_SHEON	Q8e8c2 shewanella
13	884	52.2	460	2	Q3Q816_9GAMM	Q3q816 shewanella
14	884	52.2	461	2	Q47UE0_COLP3	Q47ue0 colwellia p
15	883	52.2	454	2	Q35V62_9GAMM	Q35v62 shewanella
16	883	52.2	454	2	Q366Q8_9GAMM	Q366q8 shewanella
17	880	52.0	454	2	Q2Z4D6_9GAMM	Q2z4d6 shewanella
18	880	52.0	456	2	Q4QMS5_HAEI8	Q4qms5 haemophilus

19	879	52.0	454	2	Q3NKZ0_SHEFR	Q3nkz0 shewanella
20	878.5	51.9	454	2	Q31DM2_THICR	Q31dm2 thiomicrosp
21	877	51.8	456	1	GLMU_HAEIN	P43889 haemophilus
22	875	51.7	453	2	Q9KNH7_VIBCH	Q9knh7 vibrio chol
23	865.5	51.2	456	2	Q44KV5_CHRSL	Q44kv5 chromohalob
24	862	50.9	456	2	Q663R0_YERPS	Q663r0 yersinia ps
25	862	50.9	456	2	Q8Z9S7_YERPE	Q8z9s7 yersinia pe
26	862	50.9	458	2	Q8CZF5_YERPE	Q8czf5 yersinia pe
27	860	50.8	452	2	Q5E1N9_VIBF1	Q5e1n9 vibrio fisc
28	860	50.8	454	2	Q3EFK4_ACTSC	Q3efk4 actinobacil
29	858	50.7	456	2	Q3YVN4_SHISS	Q3yvn4 shigella so
30	858	50.7	458	2	Q3SF69_THIDA	Q3sf69 thiobacillu
31	857	50.7	453	2	Q7MGI2_VIBVY	Q7mgi2 vibrio vuln
32	857	50.7	456	2	Q8FBT3_ECOL6	Q8fbt3 escherichia
33	854	50.5	456	1	GLMU_ECO57	P0acc8 escherichia
34	854	50.5	456	1	GLMU_ECOLI	P0acc7 escherichia
35	854	50.5	456	2	Q329R9_SHIDS	Q329r9 shigella dy
36	854	50.5	456	2	Q2M848_ECOLI	Q2m848 escherichia
37	853	50.4	453	2	Q8DDG6_VIBVU	Q8ddg6 vibrio vuln
38	852.5	50.4	452	2	Q47JK2_DECAR	Q47jk2 dechloromon
39	852	50.4	454	2	Q3P1W4_9GAMM	Q3p1w4 shewanella
40	851	50.3	456	2	Q83IY3_SHIFL	Q83iy3 shigella fl
41	850	50.2	453	2	Q87KB0_VIBPA	Q87kb0 vibrio para
42	849.5	50.2	456	2	Q5QZH4_IDILO	Q5qzh4 idiomarina
43	849	50.2	454	2	Q33SJ0_9GAMM	Q33sj0 shewanella
44	849	50.2	456	2	Q31UN0_SHIBS	Q31un0 shigella bo
45	847	50.1	456	2	Q6CYJ8_ERWCT	Q6cyj8 erwinia car

<!--EndFragment-->